

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 15:47:42 ; Search time 168 Seconds
(without alignments)
43.741 Million cell updates/sec

Title: US-10-758-572-1

Perfect score: 122

Sequence: 1 GYWSWIRQPRGKEWIG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.GeneSeq.16Dec04:*

1: Genesegp1980s:*\n2: Genesegp1990s:*\n3: Genesegp2000s:*\n4: Genesegp2001s:*\n5: Genesegp2002s:*\n6: Genesegp2003as:*\n7: Genesegp2003bs:*\n8: Genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 122 | 100.0 | 19 | 5 | Aae27949 Human 16/ |
| 2 | 122 | 100.0 | 19 | 8 | Adq91214 Human com |
| 3 | 122 | 100.0 | 19 | 8 | Adt14722 Synthetic |
| 4 | 122 | 100.0 | 20 | 5 | Aae27961 Human 16/ |
| 5 | 119 | 97.5 | 19 | 5 | Aae27958 Human 16/ |
| 6 | 117 | 95.9 | 19 | 5 | Aae27956 Human 16/ |
| 7 | 116 | 95.1 | 252 | 5 | Abp45315 Human Bly |
| 8 | 115 | 94.3 | 119 | 2 | Adg96142 Single ch |
| 9 | 114 | 93.4 | 19 | 5 | Aae27959 SPA-react |
| 10 | 114 | 93.4 | 19 | 5 | Aae27960 Human 16/ |
| 11 | 114 | 93.4 | 19 | 5 | Aae27955 Human 16/ |
| 12 | 114 | 93.4 | 80 | 2 | Aaw62794 Amino aci |
| 13 | 114 | 93.4 | 97 | 2 | Aay05694 Multiple |
| 14 | 114 | 93.4 | 97 | 5 | Abg78213 Human Fv |
| 15 | 114 | 93.4 | 97 | 5 | Abg78211 Human Fv |
| 16 | 114 | 93.4 | 97 | 5 | Abg78212 Human Fv |
| 17 | 114 | 93.4 | 97 | 5 | Abg91904 Human ant |
| 18 | 114 | 93.4 | 97 | 5 | Abg91902 Human ant |
| 19 | 114 | 93.4 | 97 | 5 | Abg91903 Human ant |
| 20 | 114 | 93.4 | 97 | 6 | Abc27107 Human ger |
| 21 | 114 | 93.4 | 97 | 6 | Abc27117 Human ger |
| 22 | 114 | 93.4 | 97 | 6 | Abc27116 Human ger |
| 23 | 114 | 93.4 | 97 | 7 | Abd75646 Human pro |
| 24 | 114 | 93.4 | 97 | 7 | Add28104 Lymphoma |
| 25 | 114 | 93.4 | 97 | 7 | Add28104 Lymphoma |

| | | | | | |
|----|-----|------|-----|---|--------------------|
| 26 | 114 | 93.4 | 97 | 7 | Add28114 Lymphoma |
| 27 | 114 | 93.4 | 97 | 7 | Add28120 Lymphoma |
| 28 | 114 | 93.4 | 97 | 7 | Add28117 Lymphoma |
| 29 | 114 | 93.4 | 97 | 7 | Add10048 VEGF anti |
| 30 | 114 | 93.4 | 97 | 7 | Adf10150 Antibody |
| 31 | 114 | 93.4 | 97 | 7 | Adf09942 Antibody |
| 32 | 114 | 93.4 | 97 | 7 | Adj80323 VH gene 1 |
| 33 | 114 | 93.4 | 98 | 7 | Adj76908 Anti-IGF |
| 34 | 114 | 93.4 | 99 | 7 | Ady42967 BAA75036- |
| 35 | 114 | 93.4 | 102 | 7 | Adj32174 Human Int |
| 36 | 114 | 93.4 | 107 | 2 | Aar12267 Anti-huma |
| 37 | 114 | 93.4 | 114 | 3 | Aab01949 Anti-Id1 |
| 38 | 114 | 93.4 | 114 | 3 | Aab01950 Anti-Id1 |
| 39 | 114 | 93.4 | 114 | 3 | Aab01953 Anti-Id1 |
| 40 | 114 | 93.4 | 114 | 3 | Aab01959 High affi |
| 41 | 114 | 93.4 | 114 | 3 | Aab01952 Anti-Id1 |
| 42 | 114 | 93.4 | 114 | 3 | Aab01955 Streptati |
| 43 | 114 | 93.4 | 114 | 3 | Aab01951 Anti-Id1 |
| 44 | 114 | 93.4 | 114 | 3 | Aab01948 Wild-type |
| 45 | 114 | 93.4 | 114 | 3 | Aab01954 Anti-Id1 |

ALIGNMENTS.

RESULT 1
ID Aae27949 standard; peptide, 19 AA.

AC Aae27949;

DT 27-DEC-2002 (first entry)

DE Human 16/61d mab VH chain CDRI peptide, hCDRI.

XX Complementarity-determining region; CDR; variable heavy chain; VH; VL;

XX Variable light chain; SLF-associated response; immunosuppressive; SLF;

KW systemic lupus erythematosus; dermatological; therapy; antiinflammatory;

KM human.

OS Homo sapiens.

PN WO200267848-A2.

PD 06-SEP-2002.

PF 26-FEB-2002; 2002WO-IL000148.

PR 26-FEB-2001; 2001IL-00141647.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Mozes E;

XX WPI; 2002-698624/75.

DR New synthetic peptide useful for treating and ameliorating the clinical

PT manifestations of systemic lupus erythematosus (SLE) by modulating SLF-

PR associated responses.

XX Claim 9; Page 6; 120pp; English.

XX The invention relates to a synthetic peptide selected from a peptide of

CC 12-30 amino acid residues with a sequence of, or found within, a

CC complementarity-determining region (CDR) on the variable heavy (VH) or

CC light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The

CC composition comprising the peptide is useful for the treatment of

CC systemic lupus erythematosus (SLE) and amelioration of the clinical

CC manifestations of the disease, particularly by modulating SLF-associated

CC responses. The present sequence is human 16/61d mab VH chain CDR peptide

CC Sequence 19 AA;

SQ

Query Match 100.0%; Score 122; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYYWSWIRPPGKGEWIG 19
Db 1 GYYWSWIRPPGKGEWIG 19

RESULT 2

ADQ91214
ID ADQ91214 standard; peptide; 19 AA.

XX ADQ91214;

XX 21-OCT-2004 (first entry)

DE Human complementarity determining region 1 peptide to treat SLE Segid 1.

XX acetate salt; human; complementarity determining region 1; CDR1;

KW aqueous carrier; substituted beta-cyclodextrin; anti-inflammatory;

KW hepta-(sulfolbutyl ether)-beta-cyclodextrin; systemic lupus erythematosus; SLE;

KW dermatological; immunosuppressive; systemic lupus erythematosus; SLE;

KW interferon-gamma inhibitor;

KW transforming growth factor-beta secretion inhibitor.

XX Homo sapiens.

XX WO2004064788-A2.

XX 05-AUG-2004.

PF 14-JAN-2004; 2004WO-US000955.

XX 14-JAN-2003; 2003US-0439950P.

XX (TEVA-) TEVA PHARM IND LTD.

PA (TEVA-) TEVA PHARM USA INC.

XX Cohen-Vered S, Natfali E, Weinstein V, Gilbert A, Klinger E;

XX WPI; 2004-580637/56.

PS Claim 1; SEQ ID NO 1; 76pp; English.

XX This invention relates to a novel pharmaceutical composition comprising
CC from 0.1-20 mg/ml of an acetate salt of a human complementarity
CC determining region 1 (CDR1) peptide. Specifically, it refers to
CC parenteral formulations of this peptide, such that the composition
CC provides an aqueous carrier and a substituted beta-cyclodextrin present
CC in an amount effective to dissolve the peptide in the aqueous carrier,
CC wherein it shows a pH of between 4 and 9. The present invention further
CC describes a peptide formulation comprising the peptide and 70-170mg/ml of
CC hepta-(sulfolbutyl ether)-beta-cyclodextrin dissolved together in the
CC aqueous carrier such that the resulting pH solution is between 6.5 and
CC 8.5. These compositions have been shown to exhibit anti-inflammatory,
CC dermatological and immunosuppressive activities and accordingly can be
CC used to alleviate the symptoms of systemic lupus erythematosus (SLE) in
CC human subjects. As such, they also act as inhibitors of interferon-gamma
CC and transforming growth factor-beta secretion. This peptide sequence is
CC the human CDR1 peptide of the invention.

XX Sequence 19 AA;

Query Match 100.0%; Score 122; DB 8; Length 19;

Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYYWSWIRPPGKGEWIG 19
Db 1 GYYWSWIRPPGKGEWIG 19

RESULT 3
ADRI4722
ID ADRI4722 standard; peptide; 19 AA.

XX ADRI4722;

XX 21-OCT-2004 (first entry)

DE Synthetic peptide based on a human CDR1.

XX complementarity determining region; CDR; heavy chain; light chain;

KW monoclonal anti-DNA 16/6 idiotype antibody; 16/6 id antibody;

KW anti-DNA antibody; induces systemic lupus erythematosus; SLE.

XX Homo sapiens.

XX WO2004064787-A2.

XX 05-AUG-2004.

PF 14-JAN-2004; 2004WO-US000948.

XX 14-JAN-2003; 2003US-0439918P.

XX (TEVA-) TEVA PHARM IND LTD.

PA (TEVA-) TEVA PHARM USA INC.

XX Cohen-Vered S, Natfali E, Weinstein V, Gilbert A, Klinger E;

XX WPI; 2004-580636/56.

PS Pharmaceutical composition for treating systemic lupus erythematosus

PT (SLE), has salt of peptide corresponding to complementarity-determining

PT region of heavy/light chain of anti-DNA 16/6 id antibody that induces

PT immune response to SLE.

XX Claim 3; SEQ ID NO 6; 132pp; English.

XX The specification describes a pharmaceutical composition, comprising a
CC salt of a peptide with 12-30 consecutive amino acids having a sequence
CC corresponding to an amino acid sequence found within complementarity-
CC determining region (CDR) of the heavy or light chain of the human
CC monoclonal anti-DNA 16/6 idiotype (16/6 id) antibody, or a heavy or light
CC chain of a pathogenic anti-DNA monoclonal antibody that induces systemic
CC lupus erythematosus (SLE)-like disease response in mice. The composition
CC is useful for treating SLE and for alleviating symptoms of SLE in a human
CC subject. The present sequence represents a peptide based on a human CDR1,
CC and designated compound 1. The present peptide is used in pharmaceutical
CC compositions of the invention.

XX Sequence 19 AA;

Query Match 100.0%; Score 122; DB 8; Length 19;

Best Local Similarity 100.0%; Pred. No. 7.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYYWSWIRPPGKGEWIG 19
Db 1 GYYWSWIRPPGKGEWIG 19

RESULT 4

AAE27961
ID AAE27961 standard; peptide; 20 AA.

XX AAE27961;

DT 27-DEC-2002 (first entry)
 XX
 DE Human 16/61d mab VH chain CDR1 peptide mutant #1.
 XX
 KW Complementarity-determining region; CDR; variable heavy chain; VH; VL;
 KM variable light chain; SLF-associated response; immunosuppressive; SLF;
 KW systemic lupus erythematosus; dermatological; therapy; antiinflammatory;
 KM human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200267848-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 26-FEB-2002; 2002WO-IL000148.
 XX
 PR 26-FEB-2001; 2001IL-00141647.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Mozes E;
 XX
 DR WPI; 2002-698624/75.
 XX
 PT New synthetic peptide useful for treating and ameliorating the clinical
 PT manifestations of systemic lupus erythematosus (SLE) by modulating SLE-
 PT associated responses.
 XX
 PS Claim 8; Page 15; 120pp; English.
 XX
 CC The invention relates to a synthetic peptide selected from a peptide of
 CC 12-30 amino acid residues with a sequence of, or found within, a
 CC complementarity-determining region (CDR) on the variable heavy (VH) or
 CC light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The
 CC composition comprising the peptide is useful for the treatment of
 CC systemic lupus erythematosus (SLE) and amelioration of the clinical
 CC manifestations of the disease, particularly by modulating SLE-associated
 CC responses. The present sequence is a mutant created by addition of Thr
 CC residue to the N-terminus of human 16/61d mab VH chain CDR peptide
 CC
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 122; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWSWIRPPGKGEWIG 19
 DB 2 GYWSWIRPPGKGEWIG 20
 RESULT 5
 AAE27958
 ID AAE27958 standard; peptide; 19 AA.
 XX
 AC AAE27958;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Human 16/61d mab VH chain CDR1 peptide mutant, R8K.
 XX
 KW Complementarity-determining region; CDR; variable heavy chain; VH; VL;
 KM variable light chain; SLF-associated response; immunosuppressive; SLF;
 KW systemic lupus erythematosus; dermatological; therapy; antiinflammatory;
 KM human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN Key Location/Qualifiers
 FT MISC-difference 8
 FT

FT /note= "Wild-type Arg is replaced with Lys"
 XX
 PN WO200267848-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 26-FEB-2002; 2002WO-IL000148.
 XX
 PR 26-FEB-2001; 2001IL-00141647.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Mozes E;
 XX
 DR WPI; 2002-698624/75.
 XX
 PT New synthetic peptide useful for treating and ameliorating the clinical
 PT manifestations of systemic lupus erythematosus (SLE) by modulating SLE-
 PT associated responses.
 XX
 PS Claim 8; Page 15; 120pp; English.
 XX
 CC The invention relates to a synthetic peptide selected from a peptide of
 CC 12-30 amino acid residues with a sequence of, or found within, a
 CC complementarity-determining region (CDR) on the variable heavy (VH) or
 CC light (VL) chain of human monoclonal anti-DNA 16/61d antibody (hCDR). The
 CC composition comprising the peptide is useful for the treatment of
 CC systemic lupus erythematosus (SLE) and amelioration of the clinical
 CC manifestations of the disease, particularly by modulating SLE-associated
 CC responses. The present sequence is human 16/61d mab VH chain CDR mutant
 CC peptide
 XX
 SQ Sequence 19 AA;
 Query Match 97.5%; Score 119; DB 5; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.8e-07;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWSWIRPPGKGEWIG 19
 DB 1 GYWSWIRPPGKGEWIG 19
 RESULT 6
 AAE27956
 ID AAE27956 standard; peptide; 19 AA.
 XX
 AC AAE27956;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE Human 16/61d mab VH chain CDR1 peptide mutant, E15S.
 XX
 KW Complementarity-determining region; CDR; variable heavy chain; VH; VL;
 KM variable light chain; SLF-associated response; immunosuppressive; SLF;
 KW systemic lupus erythematosus; dermatological; therapy; antiinflammatory;
 KM human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 15 /note= "Wild-type Glu is replaced with Ser"
 FT
 PN WO200267848-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 26-FEB-2002; 2002WO-IL000148.
 XX
 PR 26-FEB-2001; 2001IL-00141647.
 XX

PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Mozes E;
XX
DR WPI; 2002-698624/75.
XX
PT New synthetic peptide useful for treating and ameliorating the clinical
PT manifestations of systemic lupus erythematosus (SLE) by modulating SLE-
PT associated responses.
XX
PS Claim 8; Page 15; 120pp; English.
XX
CC The invention relates to a synthetic peptide selected from a peptide of
CC 12-30 amino acid residues with a sequence of, or found within, a
CC complementarity-determining region (CDR) on the variable heavy (VH) or
CC light (VL) chain of human monoclonal anti-DNA 16/6id antibody (hCDR). The
CC composition comprising the peptide is useful for the treatment of
CC systemic lupus erythematosus (SLE) and amelioration of the clinical
CC manifestations of the disease, particularly by modulating SLE-associated
CC responses. The present sequence is human 16/6id mAb VH chain CDR mutant
CC peptide
XX
SQ Sequence 19 AA;
XX
Query Match 95.9%; Score 117; DB 5; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.1e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYYSWIRPPGKGEWIG 19
DB 1 GYYSWIRPPGKGEWIG 19
RESULT 7
ABP45315
ID ABP45315 standard; protein; 252 AA.
XX
AC ABP45315;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1326.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antithematic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.

XX
XX Claim 1; Page 1985-1986; 3148pp; English.
XX
PS This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
CC antithematic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 252 AA;
XX
Query Match 95.1%; Score 116; DB 5; Length 252;
Best Local Similarity 94.7%; Pred. No. 4.9e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYYSWIRPPGKGEWIG 19
DB 31 GYYSWIRPPGKGEWIG 49
RESULT 8
ADG96142
ID ADG96142 standard; protein; 252 AA.
XX
AC ADG96142;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SeqID 1326.
XX
XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; scFv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KM antiinflammatory; antiaesthetic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 1326; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to

XX Homo sapiens.
 OS
 XX
 PN WO9824893-A2.
 XX
 PD 11-JUN-1998.
 XX
 PF 03-DEC-1997; 97WO-US023091.
 XX
 PR 03-DEC-1996; 96US-00759620.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Jakobovics A, Kucheraipacti R, Klapholz S, Mendez M, Green L;
 XX
 DR WPI; 1998-333314/29.
 XX
 PT New transgenic non-human mammals - having an inactivated immunoglobulin
 PT locus and a near complete human immunoglobulin locus, used for production
 PT of human antibodies.
 XX
 PS Disclosure; Page 71; 128pp; English.
 XX
 CC AAM62793-822 represent fragments of human antibodies produced by
 CC transgenic Xenomice, created using the method of the invention. The
 CC specification describes a transgenic non-human mammal which has genome
 CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
 CC locus, so that the mammal does not display normal B-cell development. The
 CC modified genome also has an inserted human heavy chain Ig locus in
 CC germ-line configuration, the human heavy chain Ig locus comprising a human
 CC micro constant region and regulatory and switch sequences, human J-H
 CC genes, human D-H genes, and human V-H genes and an inserted human kappa
 CC light chain Ig locus in germ-line configuration, the human kappa light
 CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
 CC and V-kappa genes, where the number of V-H and V-kappa genes inserted are
 CC selected to restore normal B-cell development in the mammal. The
 CC transgenic animals have a near complete human Ig locus, including both a
 CC human heavy chain locus and a human kappa light chain locus. They can be
 CC used for the production of human antibodies when exposed to particular
 CC antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
 CC will produce antibodies to IL-8, EGFR or TNF- alpha respectively
 XX
 SQ Sequence 80 AA;
 Query Match 93.4%; Score 114; DB 2; Length 80;
 Best Local Similarity 94.7%; Pred. No. 2.8e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYWSMTROPKGEWIG 19
 |||||
 14 GYWSMTROPKGEWIG 32
 RESULT 14
 AAY05694
 ID AAY05694 standard; protein, 97 AA.
 XX
 AC AAY05694;
 XX
 DT 19-JUN-1999 (first entry)
 XX
 DE Multiple sclerosis patient CSF B-cell VH region (clone 4d76).
 XX
 KM Multiple sclerosis; cerebrospinal fluid; CSF; B-cell;
 KM heavy chain variable region; VH gene; somatic hypermutation;
 XX
 OS B-cell clonality; RA gene; diagnosis; human.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Region 1. .30
 FT Location/Qualifiers
 FT /label= FR1
 FT Misc-difference 8

FT /note= "encoded by GGC"
 FT Misc-difference 13
 FT /note= "replaces Gln of RA"
 FT Misc-difference 14
 FT /note= "encoded by CCT"
 FT Misc-difference 23
 FT /note= "replaces Gly of RA"
 FT Misc-difference 25
 FT /note= "replaces Phe of RA"
 FT Misc-difference 30
 FT /note= "replaces Gly of RA"
 FT Region 31. .36
 FT /label= CDR1
 FT Misc-difference 31
 FT /note= "replaces Gly of RA"
 FT Misc-difference 32
 FT /note= "replaces Phe of RA"
 FT Region 37. .50
 FT /label= FR2
 FT Region 51. .66
 FT /label= CDR2
 FT Misc-difference 56
 FT /note= "replaces Asn of RA"
 FT Misc-difference 57
 FT /note= "replaces Ser of RA"
 FT Misc-difference 58
 FT /note= "replaces Lys of RA"
 FT Region 67. .97
 FT /label= FR3
 FT Misc-difference 71
 FT /note= "replaces Leu of RA"
 FT Misc-difference 81
 FT /note= "replaces Arg of RA"
 XX
 PN WO9915696-A1.
 XX
 PD 01-APR-1999.
 XX
 PF 17-SEP-1998; 98WO-CA000873.
 XX
 PR 19-SEP-1997; 97CA-02216595.
 PR 04-NOV-1997; 97CA-02220245..
 XX
 PA (QINV/) QIN Y.
 XX
 PI QIN Y;
 XX
 DR WPI; 1999-276985/23.
 DR N-PSDB; AAX25318.
 XX
 PT Determination of B-cell clonality by amplification or enzymatic
 PT digestion.
 XX
 PS Disclosure; Fig 9D; 67pp; English.
 XX
 CC This sequence represents a heavy chain variable region (VH) as predicted
 CC from DNA of dominant clone 4d76 of B-cells taken from the cerebrospinal
 CC fluid (CSF) of a multiple sclerosis (MS) patient. Sequences of VH of CSF
 CC B-cells were obtained from 4 MS patients (see AAX25316-19). Differences
 CC in nucleotide and predicted amino acid (see AAY05691-94) sequences were
 CC compared with the closest known germ-line VH genes, for 4d76, this was RA.
 CC The results provided direct evidence that intrathecal clonally expanded B
 CC -cells from the CSF of MS patients are hypermutated postgerminal centre
 CC antibody-forming or memory lymphocytes that have undergone antigen
 CC selection. This finding implicates an important pathogenic pathway for
 CC the development of demyelination in CNS of MS. The invention provides
 CC assay kits for determining B-cell or T-cell clonality. This technology
 CC allows the establishment of clonal specific RNA library from pathogenic
 CC cells in the CNS of patients, which is important for further
 CC understanding of the role of antigen(s) in the cause of B-cell clonal
 CC expansion, and towards developing antigen specific therapeutic strategy
 XX
 SQ Sequence 97 AA;

Search completed: April 25, 2005, 16:02:48
 Job time : 170 secs

Query Match 93.4%; Score 114; DB 2; Length 97;
 Best Local Similarity 94.7%; Pred. No. 3.4e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRPPGKGEWIG 19
 |||||
 Db 31 GYWSWIRPPGKGEWIG 49

RESULT 15

ABG78213
 ID ABG78213 standard; protein; 97 AA.

XX ABG78213;

XX 15-NOV-2002 (first entry)

XX Human Fv molecule hypervariable region related peptide #88.

XX Human Fv molecule; hypervariable region; single chain Fv; cyrostatic;

KW disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;

KW lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia.

XX Homo sapiens.

XX NO200259264-A2.

XX 01-AUG-2002.

XX 31-DEC-2001; 2001WO-US049440.

XX 29-DEC-2000; 2000US-00751181.

XX (BIOT-) BIO-TECHNOLOGY GEN CORP.

XX Hagai Y, Lazarovits J, Guy R, Lipschitz O, Szanton E, Levanon A;

XX Plaksin D, Peretz T;

XX WPI; 2002-619166/66.

XX Novel peptide/polypeptide for cancer therapy has Fv molecule, construct

XX PT or fragment, or construct of fragment with enhanced binding

XX PT characteristics so as to selectively bind target cell in favor of other

XX cells.

XX Claim 13; Page 193-194, 232pp; English.

XX The invention relates to a peptide or polypeptide comprising an Fv

XX molecule, a construct or fragments or a construct of a fragment with

XX enhanced binding characteristics which selectively and/or specifically

XX binds to a target cell in favour of other cells, where binding is

XX primarily determined by a first hypervariable region and Fv is a single

XX chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in

XX association with or attached, coupled, combined, linked or fused to a

XX pharmaceutical agent, is useful in the manufacture of a medicament, where

XX the medicament has activity against a diseased cell, preferably a cancer

XX cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,

XX myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an

XX acute myeloid leukaemia cell). The peptide is also useful for preparing a

XX composition for use in inhibiting the growth of a diseased or cancer

XX cell. This sequence represents a human Fv molecule hypervariable region

XX related peptide of the invention

XX SQ Sequence 97 AA;

Query Match 93.4%; Score 114; DB 5; Length 97;
 Best Local Similarity 94.7%; Pred. No. 3.4e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRPPGKGEWIG 19
 |||||
 Db 31 GYWSWIRPPGKGEWIG 49

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: April 25, 2005, 16:00:09 ; Search time 42 Seconds
(without alignments)
33.770 Million cell updates/sec

Title: US-10-758-572-1
Perfect score: 122
Sequence: 1 GYWSWIRQPGKGEWIG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA:*
2: /cgn2_6/ptodata/1/aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/1/aa/6B.COMB.pep:*
6: /cgn2_6/ptodata/1/aa/PTCUS.COMB.pep:*
7: /cgn2_6/ptodata/1/aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 115 | 94.3 | 119 | 2 | US-08-428-197-16 |
| 2 | 115 | 94.3 | 119 | 5 | PCT-US93-10555-16 |
| 3 | 114 | 93.4 | 116 | 3 | US-08-545-809A-118 |
| 4 | 114 | 93.4 | 123 | 3 | US-08-793-450-4 |
| 5 | 114 | 93.4 | 139 | 4 | US-09-203-768A-2 |
| 6 | 114 | 93.4 | 472 | 3 | US-08-793-450-8 |
| 7 | 114 | 93.4 | 473 | 4 | US-09-049-672A-4 |
| 8 | 110 | 90.2 | 117 | 4 | US-09-720-493-2 |
| 9 | 110 | 90.2 | 124 | 1 | US-08-478-039-78 |
| 10 | 110 | 90.2 | 124 | 1 | US-08-476-349A-78 |
| 11 | 108 | 88.5 | 76 | 3 | US-08-851-362D-22 |
| 12 | 108 | 88.5 | 96 | 3 | US-08-851-362D-35 |
| 13 | 108 | 88.5 | 97 | 3 | US-08-851-362D-33 |
| 14 | 108 | 88.5 | 98 | 1 | US-08-478-039-75 |
| 15 | 108 | 88.5 | 98 | 1 | US-08-476-349A-75 |
| 16 | 108 | 88.5 | 116 | 3 | US-08-545-809A-140 |
| 17 | 108 | 88.5 | 117 | 3 | US-08-851-362D-48 |
| 18 | 108 | 88.5 | 117 | 4 | US-09-232-290-47 |
| 19 | 108 | 88.5 | 118 | 3 | US-08-545-809A-142 |
| 20 | 108 | 88.5 | 118 | 3 | US-08-851-362D-47 |
| 21 | 108 | 88.5 | 118 | 4 | US-09-025-769B-25 |
| 22 | 108 | 88.5 | 118 | 4 | US-09-490-070A-25 |
| 23 | 108 | 88.5 | 118 | 4 | US-09-490-153-25 |
| 24 | 108 | 88.5 | 118 | 4 | US-09-490-324-25 |
| 25 | 108 | 88.5 | 119 | 2 | US-08-652-816A-10 |
| 26 | 108 | 88.5 | 119 | 3 | US-09-025-769B-39 |
| 27 | 108 | 88.5 | 119 | 3 | US-09-025-769B-65 |

| | | | | | | |
|----|-----|------|-----|---|--------------------|-------------------|
| 28 | 108 | 88.5 | 119 | 4 | US-09-490-070A-39 | Sequence 39, Appl |
| 29 | 108 | 88.5 | 119 | 4 | US-09-490-070A-65 | Sequence 65, Appl |
| 30 | 108 | 88.5 | 119 | 4 | US-09-490-153-39 | Sequence 39, Appl |
| 31 | 108 | 88.5 | 119 | 4 | US-09-490-153-65 | Sequence 65, Appl |
| 32 | 108 | 88.5 | 119 | 4 | US-09-490-324-39 | Sequence 39, Appl |
| 33 | 108 | 88.5 | 119 | 4 | US-09-490-324-65 | Sequence 65, Appl |
| 34 | 108 | 88.5 | 120 | 4 | US-09-424-840B-20 | Sequence 20, Appl |
| 35 | 108 | 88.5 | 139 | 4 | US-09-471-276-837 | Sequence 837, App |
| 36 | 108 | 88.5 | 219 | 3 | US-09-460-384-37 | Sequence 37, Appl |
| 37 | 108 | 88.5 | 244 | 3 | US-08-918-148-79 | Sequence 79, Appl |
| 38 | 108 | 88.5 | 244 | 4 | US-09-138-091A-77 | Sequence 77, Appl |
| 39 | 106 | 86.9 | 140 | 4 | US-09-471-276-850 | Sequence 850, App |
| 40 | 105 | 86.1 | 76 | 3 | US-08-851-362D-19 | Sequence 19, Appl |
| 41 | 105 | 86.1 | 76 | 4 | US-09-472-087-85 | Sequence 85, Appl |
| 42 | 105 | 86.1 | 118 | 3 | US-08-545-809A-116 | Sequence 116, App |
| 43 | 105 | 86.1 | 150 | 4 | US-09-582-337-14 | Sequence 14, Appl |
| 44 | 104 | 85.2 | 111 | 4 | US-09-471-276-840 | Sequence 840, App |
| 45 | 104 | 85.2 | 118 | 3 | US-08-545-809A-123 | Sequence 123, App |

ALIGNMENTS

```

RESULT 1
US-08-428-197-16
; Sequence 16, Application US/08428197
; Patent No. 5691438
;
; GENERAL INFORMATION:
; APPLICANT: SILVERMAN, GREGG J.
; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
; NUMBER OF INVENTION: 51
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10555
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: FD-2630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5110
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: LBS
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..119
; US-08-428-197-16

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Query Match 94.3%; Score 115; DB 2; Length 119;
Best Local Similarity 89.5%; Pred. No. 8.3e-08;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
|||||:|||||
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 2
PCT-US93-10555-16
; Sequence 16, Application PC/TUS9310555
; GENERAL INFORMATION:

;; APPLICANT: SILVERMAN, GREGG J.
;; TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
;; TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
;; TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
;; TITLE OF INVENTION: THEREOF
;; NUMBER OF SEQUENCES: 51
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Spensley Horn Jubas & Lubitz
;; STREET: 1880 Century Park East - Suite 500
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: USA

;; ZIP: 90067
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/10555
;; FILING DATE: 29-OCT-1993
;; CLASSIFICATION:

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Howells, Stacy L.
;; REGISTRATION NUMBER: 34,842
;; REFERENCE/DOCKET NUMBER: PD-2630
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 455-5110
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; IMMEDIATE SOURCE:
;; CLONE: LBS
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..119
PCT-US93-10555-16

Query Match 94.3%; Score 115; DB 5; Length 119;
Best Local Similarity 89.5%; Pred. No. 8.3e-08;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
|||||:|||||
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 3

US-08-545-809A-118
; Sequence 118, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko

;; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;; NUMBER OF SEQUENCES: 145
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson, P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: US

;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: Windows95
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/545,809A
;; FILING DATE: 27-MAR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/JP93/00603
;; FILING DATE: 10-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Freeman, John W.
;; REGISTRATION NUMBER: 29,066
;; REFERENCE/DOCKET NUMBER: 06501/004001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 118:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 116 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-545-809A-118

Query Match 93.4%; Score 114; DB 3; Length 116;
Best Local Similarity 94.7%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
|||||:|||||
Db 50 GYWSWIRPPGKGEWIG 68

RESULT 4
US-08-793-450-4
; Sequence 4, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABIBI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHSUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA

;; ZIP: 22202
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/793,450

FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-4

Query Match 93.4%; Score 114; DB 3; Length 123;
Best Local Similarity 94.7%; Pred. No. 1.2e-07;
Matches 18; Conservative 1; Indels 0; Gaps 0;

Oy 1 GYWSWIRPPGKGEWIG 19
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 5
US-09-203-768A-2
Sequence 2, Application US/09203768A
Patent No. 6787638
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Watkins, Jeffrey D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: of use
FILE REFERENCE: P-IX 2947
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 139
TYPE: PRT
ORGANISM: Homo sapiens
US-09-203-768A-2

Query Match 93.4%; Score 114; DB 4; Length 139;
Best Local Similarity 94.7%; Pred. No. 1.3e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYWSWIRPPGKGEWIG 19
Db 50 GYWSWIRPPGKGEWIG 68

RESULT 6
US-08-793-450-8
Sequence 8, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITE, CRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHABIH, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-8

Query Match 93.4%; Score 114; DB 3; Length 472;
Best Local Similarity 94.7%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYWSWIRPPGKGEWIG 19
Db 50 GYWSWIRPPGKGEWIG 68

RESULT 7
US-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HERewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ceirone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE//DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
;
;
;
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTCTUT01
; CLONE: 1513264
;
US-09-049-672A-4
;
Query Match 93.4%; Score 114; DB 3; Length 473;
Best Local Similarity 94.7%; Pred. No. 4.5e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYYWSWIRPPGKGLEWIG 19
Db 52 GYYWSWIRPPGKGLEWIG 70

RESULT 8
US-09-720-493-2
; Sequence 2, Application US/09720493
; Patent No. 6827925
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Williams, Andrew J
; APPLICANT: Tempest, Philip R
; APPLICANT: Holter, Thor L
; APPLICANT: Main, Sarah H
; APPLICANT: Jackson, Helen
; APPLICANT: Daromola, Olalekan
; TITLE OF INVENTION: Improvements relating to antibodies
; FILE REFERENCE: AHB/CP575333
; CURRENT APPLICATION NUMBER: US/09/720,493
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: GB 9814383.7
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-720-493-2
;
Query Match 90.2%; Score 110; DB 4; Length 117;
Best Local Similarity 89.5%; Pred. No. 3.6e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYYWSWIRPPGKGLEWIG 19
Db 32 GYYWSWIRPPGKGLEWIG 50

RESULT 9
US-08-478-039-78
; Sequence 78, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; APPLICANT: Raab, Ronald W.
```

```

; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS: 114
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teakin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE//DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Monkey
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH4 clone 4-16
;
US-08-478-039-78
;
Query Match 90.2%; Score 110; DB 1; Length 124;
Best Local Similarity 89.5%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYYWSWIRPPGKGLEWIG 19
Db 33 GYYWSWIRPPGKGLEWIG 51

RESULT 10
US-08-476-349A-78
; Sequence 78, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
```

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STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH4 clone 4-16
US-08-476-349A-78

Query Match      90.2%; Score 110; DB 1; Length 124;
Best Local Similarity 89.5%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYWSWIRPPGKGLEWIG 19
Db      33 GYWSWIRPPGKGLEWIG 51

RESULT 11
US-08-851-362D-22
; Sequence 22, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
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US-08-851-362D-22
Query Match      88.5%; Score 108; DB 3; Length 76;
Best Local Similarity 94.4%; Pred. No. 4.2e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 YYWSWIRPPGKGLEWIG 19
Db      11 YYWSWIRPPGKGLEWIG 28

RESULT 12
US-08-851-362D-35
; Sequence 35, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 96
; TYPE: PRT
; ORGANISM: human
US-08-851-362D-35

Query Match      88.5%; Score 108; DB 3; Length 96;
Best Local Similarity 94.4%; Pred. No. 5.4e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 YYWSWIRPPGKGLEWIG 19
Db      11 YYWSWIRPPGKGLEWIG 28

RESULT 13
US-08-851-362D-33
; Sequence 33, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 97
; TYPE: PRT
; ORGANISM: human
US-08-851-362D-33

Query Match      88.5%; Score 108; DB 3; Length 97;
Best Local Similarity 94.4%; Pred. No. 5.4e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 YYWSWIRPPGKGLEWIG 19
Db      11 YYWSWIRPPGKGLEWIG 28
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RESULT 14
US-08-478-039-75
; Sequence 75: Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teekin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH4 consensus
; US-08-478-039-75

Query Match      88.5%; Score 108; DB 1; Length 98;
Best Local Similarity 94.4%; Pred. No. 5.5e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 YVWSWIRPPGKGLEWIG 19
Db      33 YVWSWIRPPGKGLEWIG 50

RESULT 15
US-08-476-349A-75
; Sequence 75: Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
```

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APPLICANT: Hanna, Nabil
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teekin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VH4 consensus
; US-08-476-349A-75

Query Match      88.5%; Score 108; DB 1; Length 98;
Best Local Similarity 94.4%; Pred. No. 5.5e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 YVWSWIRPPGKGLEWIG 19
Db      33 YVWSWIRPPGKGLEWIG 50

Search completed: April 25, 2005, 16:15:37
Job time : 43 secs
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OM protein - protein search, using sw model

Run on: April 25, 2005, 16:06:05 ; Search time 134 Seconds
(without alignments)
47.187 Million cell updates/sec

Title: US-10-758-572-1

Perfect score: 122
Sequence: 1 GYWSWIRQPRGKEWIG 19

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pcp.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|--------------------------------------|
| 1 | 122 | 100.0 | 19 | US-10-468-924-6 Sequence 6, Appl1 |
| 2 | 122 | 100.0 | 19 | US-10-758-572-1 Sequence 1, Appl1 |
| 3 | 122 | 100.0 | 19 | US-10-758-397-6 Sequence 6, Appl1 |
| 4 | 122 | 100.0 | 19 | US-10-758-397-18 Sequence 18, Appl1 |
| 5 | 122 | 100.0 | 20 | US-10-468-924-18 Sequence 18, Appl1 |
| 6 | 119 | 97.5 | 19 | US-10-468-924-15 Sequence 15, Appl1 |
| 7 | 117 | 95.9 | 19 | US-10-468-924-13 Sequence 13, Appl1 |
| 8 | 116 | 95.1 | 19 | US-10-468-924-14 Sequence 14, Appl1 |
| 9 | 116 | 95.1 | 252 | US-09-880-748-1326 Sequence 1326, Ap |
| 10 | 116 | 95.1 | 252 | US-10-293-418-1326 Sequence 1326, Ap |
| 11 | 114 | 93.4 | 19 | US-10-468-924-12 Sequence 12, Appl1 |
| 12 | 114 | 93.4 | 19 | US-10-468-924-16 Sequence 16, Appl1 |
| 13 | 114 | 93.4 | 19 | US-10-468-924-17 Sequence 17, Appl1 |

| | | | | | | |
|----|-----|------|-----|----|---------------------|--------------------|
| 14 | 114 | 93.4 | 80 | 14 | US-10-078-958-2 | Sequence 2, Appl1 |
| 15 | 114 | 93.4 | 97 | 14 | US-10-194-975-40 | Sequence 40, Appl1 |
| 16 | 114 | 93.4 | 97 | 14 | US-10-194-975-49 | Sequence 49, Appl1 |
| 17 | 114 | 93.4 | 97 | 14 | US-10-194-975-50 | Sequence 50, Appl1 |
| 18 | 114 | 93.4 | 97 | 15 | US-10-308-817-83 | Sequence 83, Appl1 |
| 19 | 114 | 93.4 | 97 | 15 | US-10-032-0378-86 | Sequence 86, Appl1 |
| 20 | 114 | 93.4 | 97 | 15 | US-10-032-0378-86 | Sequence 87, Appl1 |
| 21 | 114 | 93.4 | 97 | 15 | US-10-032-0378-87 | Sequence 88, Appl1 |
| 22 | 114 | 93.4 | 97 | 15 | US-10-029-988B-86 | Sequence 88, Appl1 |
| 23 | 114 | 93.4 | 97 | 15 | US-10-029-988B-87 | Sequence 88, Appl1 |
| 24 | 114 | 93.4 | 97 | 15 | US-10-029-988B-88 | Sequence 88, Appl1 |
| 25 | 114 | 93.4 | 97 | 15 | US-10-032-423A-86 | Sequence 88, Appl1 |
| 26 | 114 | 93.4 | 97 | 15 | US-10-032-423A-86 | Sequence 88, Appl1 |
| 27 | 114 | 93.4 | 97 | 15 | US-10-032-423A-88 | Sequence 88, Appl1 |
| 28 | 114 | 93.4 | 97 | 15 | US-10-453-698-83 | Sequence 88, Appl1 |
| 29 | 114 | 93.4 | 97 | 15 | US-10-029-926B-86 | Sequence 88, Appl1 |
| 30 | 114 | 93.4 | 97 | 15 | US-10-029-926B-87 | Sequence 88, Appl1 |
| 31 | 114 | 93.4 | 97 | 15 | US-10-029-926B-88 | Sequence 88, Appl1 |
| 32 | 114 | 93.4 | 97 | 16 | US-10-379-392-47 | Sequence 47, Appl1 |
| 33 | 114 | 93.4 | 102 | 10 | US-09-972-656-128 | Sequence 128, App |
| 34 | 114 | 93.4 | 114 | 14 | US-10-027-725A-9 | Sequence 9, Appl1 |
| 35 | 114 | 93.4 | 114 | 17 | US-10-733-532-128 | Sequence 128, App |
| 36 | 114 | 93.4 | 116 | 14 | US-10-072-301-38 | Sequence 38, Appl1 |
| 37 | 114 | 93.4 | 116 | 14 | US-10-071-866-38 | Sequence 38, Appl1 |
| 38 | 114 | 93.4 | 116 | 15 | US-10-360-828-38 | Sequence 38, Appl1 |
| 39 | 114 | 93.4 | 116 | 15 | US-10-338-366-6 | Sequence 6, Appl1 |
| 40 | 114 | 93.4 | 117 | 15 | US-10-309-762-127 | Sequence 127, App |
| 41 | 114 | 93.4 | 117 | 9 | US-09-864-761-44315 | Sequence 44315, A |
| 42 | 114 | 93.4 | 118 | 15 | US-10-371-942-90 | Sequence 90, Appl1 |
| 43 | 114 | 93.4 | 118 | 15 | US-10-388-214A-36 | Sequence 36, Appl1 |
| 44 | 114 | 93.4 | 119 | 14 | US-10-078-958-3 | Sequence 3, Appl1 |
| 45 | 114 | 93.4 | 120 | 15 | US-10-309-762-128 | Sequence 128, App |

ALIGNMENTS

RESULT 1
US-10-468-924-6
; Sequence 6, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Compris
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human
US-10-468-924-6

Query Match 100.0%; Score 122; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWSWIRQPRGKEWIG 19
|||
Db 1 GYWSWIRQPRGKEWIG 19

RESULT 2
US-10-758-572-1
; Sequence 1, Application US/10758572
; Publication No. US20040180059A1
; GENERAL INFORMATION:

```
; APPLICANT: Cohen-Vered, Sharon
; APPLICANT: Natfali, Esmera
; APPLICANT: Weinstein, Vera
; APPLICANT: Gilbert, Adrian
; APPLICANT: Klingert, Ely
; TITLE OF INVENTION: PARENTERAL FORMULATIONS OF A PEPTIDE FOR THE TREATMENT OF SYSTEMIC
; FILE REFERENCE: 2609/68518-A
; CURRENT APPLICATION NUMBER: US/10/758,572
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide of 19 amino acids based on the
; OTHER INFORMATION: complementarity-determining region 1 (CDR1) of the
; OTHER INFORMATION: human anti-dsDNA mAb denoted 16/6 Id
US-10-758-572-1
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Query Match          100.0%; Score 122; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GYWSWIRPPGKGEEMIG 19
        |||
Db       1 GYWSWIRPPGKGEEMIG 19
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RESULT 3
US-10-758-397-6
; Sequence 6, Application US/10758397
; Publication No. US2005008634A1
; GENERAL INFORMATION:
; APPLICANT: Cohen-Vered, et al., Sharon
; TITLE OF INVENTION: PARENTERAL FORMULATIONS OF PEPTIDES FOR THE TREATMENT OF SYSTEMIC
; FILE REFERENCE: 2609/68811-A
; CURRENT APPLICATION NUMBER: US/10/758,397
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide based on CDR of mouse autoantibody
US-10-758-397-6
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Query Match          100.0%; Score 122; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GYWSWIRPPGKGEEMIG 19
        |||
Db       1 GYWSWIRPPGKGEEMIG 19
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RESULT 4
US-10-758-397-18
; Sequence 18, Application US/10758397
; Publication No. US2005008634A1
; GENERAL INFORMATION:
; APPLICANT: Cohen-Vered, et al., Sharon
; TITLE OF INVENTION: PARENTERAL FORMULATIONS OF PEPTIDES FOR THE TREATMENT OF SYSTEMIC
; FILE REFERENCE: 2609/68811-A
; CURRENT APPLICATION NUMBER: US/10/758,397
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 18
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide based on the complementarity-determining region
; OTHER INFORMATION: 1 of human anti-dsDNA mAb denoted 16/6 Id
US-10-758-397-18
```

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Query Match          100.0%; Score 122; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GYWSWIRPPGKGEEMIG 19
        |||
Db       1 GYWSWIRPPGKGEEMIG 19
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RESULT 5
US-10-468-924-18
; Sequence 18, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; APPLICANT: MOZES, Edna
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Compris
; TITLE OF INVENTION: for the Treatment of Systemic Lupus Erythematosus
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Thr Gly, Xaa(8) is
; OTHER INFORMATION: Yg, Xaa(10) is Pro, Xaa(12) is Gly, Xaa(13) is Lys, and Xaa(15)
; OTHER INFORMATION: s Gly.
US-10-468-924-18
```

```
Query Match          100.0%; Score 122; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GYWSWIRPPGKGEEMIG 19
        |||
Db       2 GYWSWIRPPGKGEEMIG 20
```

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RESULT 6
US-10-468-924-15
; Sequence 15, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; APPLICANT: MOZES, Edna
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Compris
; TITLE OF INVENTION: for the Treatment of Systemic Lupus Erythematosus
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 19
; TYPE: PRT
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Lys,
OTHER INFORMATION: Xaa(10) is Pro, Xaa(12) is Gly, Xaa(13) is Lys, and Xaa(15) is Gl
US-10-468-924-15

Query Match 97.5%; Score 119; DB 16; Length 19;

Best Local Similarity 94.7%; Pred. No. 4.3e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWSWIRQPPGKGSEWIG 19
Db 1 GYWSWIRQPPGKGSEWIG 19

RESULT 7
US-10-468-924-13

Sequence 13, Application US/10468924
Publication No. US20040127408A1

GENERAL INFORMATION:

APPLICANT: YEDA Research and Development Co. Ltd

APPLICANT: MOZES, Edna

TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Comprisi

FILE REFERENCE: TEVA-003 PCT

CURRENT FILING DATE: 2003-08-21

PRIOR FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 13

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Arg,

OTHER INFORMATION: Xaa(10) is Pro, Xaa(12) is Gly, Xaa(13) is Lys, and Xaa(15) is Se

US-10-468-924-13

Query Match 95.9%; Score 117; DB 16; Length 19;

Best Local Similarity 94.7%; Pred. No. 7.6e-08; Mismatches 1; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRQPPGKGSEWIG 19
Db 1 GYWSWIRQPPGKGSEWIG 19

RESULT 8
US-10-468-924-14

Sequence 14, Application US/10468924
Publication No. US20040127408A1

GENERAL INFORMATION:

APPLICANT: YEDA Research and Development Co. Ltd

APPLICANT: MOZES, Edna

TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Comprisi

FILE REFERENCE: TEVA-003 PCT

CURRENT FILING DATE: 2003-08-21

PRIOR FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 14

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Arg,

OTHER INFORMATION: Xaa(10) is Pro, Xaa(12) is Gly, Xaa(13) is Asp, and Xaa(15) is C
OTHER INFORMATION: u.
US-10-468-924-14

Query Match 95.1%; Score 116; DB 16; Length 19;

Best Local Similarity 94.7%; Pred. No. 1e-07; Mismatches 1; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRQPPGKGSEWIG 19
Db 1 GYWSWIRQPPGKGSEWIG 19

RESULT 9
US-09-880-748-1326

Sequence 1326, Application US/09880748
Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23

CURRENT FILING DATE: 2001-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

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PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

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; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1326
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1326

Query Match          95.1%; Score 116; DB 15; Length 252;
Best Local Similarity 94.7%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
   |||||
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 11
US-10-468-924-12
; Sequence 12, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; APPLICANT: MOZES, Edna
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Comprisi
; TITLE OF INVENTION: for the Treatment of Systemic Lupus Erythematosus
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Arg,
; OTHER INFORMATION: Xaa(10) is Pro, Xaa(12) is Gly, Xaa(13) is Lys, and Xaa(15) is Le
; OTHER INFORMATION: u.
US-10-468-924-12

Query Match          93.4%; Score 114; DB 16; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
   |||||
Db 1 GYWSWIRPPGKGEWIG 19

RESULT 12
US-10-468-924-16
; Sequence 16, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; APPLICANT: MOZES, Edna
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Comprisi
; TITLE OF INVENTION: for the Treatment of Systemic Lupus Erythematosus
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 19
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Arg,
; OTHER INFORMATION: Xaa(10) is Ser, Xaa(12) is Gly, Xaa(13) is Lys, and Xaa(15) is G
; OTHER INFORMATION: u.
US-10-468-924-16

Query Match          93.4%; Score 114; DB 16; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
   |||||
Db 1 GYWSWIRPPGKGEWIG 19

RESULT 13
US-10-468-924-17
; Sequence 17, Application US/10468924
; Publication No. US20040127408A1
; GENERAL INFORMATION:
; APPLICANT: YEDA Research and Development Co. Ltd
; APPLICANT: MOZES, Edna
; TITLE OF INVENTION: Synthetic Human Peptides and Pharmaceutical Compositions Comprisi
; TITLE OF INVENTION: for the Treatment of Systemic Lupus Erythematosus
; FILE REFERENCE: TEVA-003 PCT
; CURRENT APPLICATION NUMBER: US/10/468,924
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: IL 141647
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide of SEQ ID NO: 11 wherein Xaa(1) is Gly, Xaa(8) is Arg,
; OTHER INFORMATION: Xaa(10) is Pro, Xaa(12) is Glu, Xaa(13) is Lys, and Xaa(15) is G
; OTHER INFORMATION: u.
US-10-468-924-17

Query Match          93.4%; Score 114; DB 16; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
   |||||
Db 1 GYWSWIRPPGKGEWIG 19

RESULT 14
US-10-078-958-2
; Sequence 2, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KOCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN IG LOCI INCLUDING
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 80
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-078-958-2

Query Match 93.4%; Score 114; DB 14; Length 80;
Best Local Similarity 94.7%; Pred. No. 6.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYWSWIRQPPGKGEWIG 19
|||
Db 14 GYWSWIRQPPGKGEWIG 32

RESULT 15
US-10-194-975-40
; Sequence 40, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Roore, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-40

Query Match 93.4%; Score 114; DB 14; Length 97;
Best Local Similarity 94.7%; Pred. No. 7.6e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYWSWIRQPPGKGEWIG 19
|||
Db 31 GYWSWIRQPPGKGEWIG 49

Search completed: April 25, 2005, 16:18:45
Job time : 135 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 15:56:43 ; Search time 39 Seconds

(without alignments)
46.875 Million cell updates/sec

Title: US-10-758-572-1

Perfect score: 122
Sequence: 1 GYWSWIRQPRKGEWIG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.79:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 117 | 95.9 | 143 | 2 | B49028 |
| 2 | 114 | 93.4 | 97 | 2 | S26898 |
| 3 | 114 | 93.4 | 97 | 2 | S26806 |
| 4 | 114 | 93.4 | 97 | 2 | S26805 |
| 5 | 114 | 93.4 | 97 | 2 | S14474 |
| 6 | 114 | 93.4 | 106 | 2 | S37454 |
| 7 | 114 | 93.4 | 122 | 2 | UJ0047 |
| 8 | 114 | 93.4 | 126 | 2 | S47010 |
| 9 | 114 | 93.4 | 140 | 2 | S78052 |
| 10 | 114 | 93.4 | 140 | 2 | A49045 |
| 11 | 111 | 91.0 | 146 | 1 | G1HMH2 |
| 12 | 110 | 90.2 | 98 | 2 | S26902 |
| 13 | 110 | 90.2 | 98 | 2 | S12421 |
| 14 | 110 | 90.2 | 123 | 3 | S30530 |
| 15 | 110 | 90.2 | 129 | 1 | DHUMA |
| 16 | 110 | 90.2 | 140 | 2 | A24770 |
| 17 | 109 | 89.3 | 137 | 2 | S34149 |
| 18 | 108 | 88.5 | 39 | 2 | S26937 |
| 19 | 108 | 88.5 | 97 | 2 | S26906 |
| 20 | 108 | 88.5 | 97 | 2 | G34964 |
| 21 | 108 | 88.5 | 97 | 2 | S12416 |
| 22 | 108 | 88.5 | 99 | 2 | S26802 |
| 23 | 108 | 88.5 | 99 | 2 | S26803 |
| 24 | 108 | 88.5 | 105 | 2 | S44125 |
| 25 | 108 | 88.5 | 114 | 2 | S12667 |
| 26 | 108 | 88.5 | 116 | 2 | B26340 |
| 27 | 108 | 88.5 | 118 | 2 | A26340 |
| 28 | 108 | 88.5 | 140 | 2 | I37782 |
| 29 | 108 | 88.5 | 146 | 2 | S09711 |

| | | | | | | |
|----|-----|------|-----|---|--------|--------------------|
| 30 | 108 | 88.5 | 155 | 2 | S31512 | Ig heavy chain - h |
| 31 | 108 | 88.5 | 155 | 2 | S31511 | Ig heavy chain - h |
| 32 | 108 | 88.5 | 231 | 2 | B23746 | Ig Fab region IV-J |
| 33 | 105 | 86.1 | 97 | 2 | PL0118 | Ig heavy chain V-I |
| 34 | 105 | 86.1 | 97 | 2 | JH0428 | Ig gamma chain V r |
| 35 | 105 | 86.1 | 99 | 2 | S26801 | Ig heavy chain V r |
| 36 | 105 | 86.1 | 99 | 2 | S26807 | Ig heavy chain V r |
| 37 | 105 | 86.1 | 99 | 2 | S26899 | Ig heavy chain V r |
| 38 | 105 | 86.1 | 116 | 2 | S37456 | Ig mu chain - huma |
| 39 | 104 | 85.2 | 39 | 2 | S26939 | Ig heavy chain V r |
| 40 | 104 | 85.2 | 99 | 2 | S26800 | Ig heavy chain V r |
| 41 | 104 | 85.2 | 99 | 2 | S12412 | Ig heavy chain V r |
| 42 | 104 | 85.2 | 99 | 2 | S12418 | Ig heavy chain V r |
| 43 | 104 | 85.2 | 100 | 2 | S78056 | Ig heavy chain V r |
| 44 | 104 | 85.2 | 110 | 2 | S44110 | Ig heavy chain V-D |
| 45 | 104 | 85.2 | 124 | 2 | S31684 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1
B49028
Ig heavy chain V-IV region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: B49028
R:Simmons, E.; Kentner, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schu
Eur. J. Immunol. 21, 2355-2363, 1991
A:Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lympho
A:Reference number: A49028; MUID:92008140; PMID:1915549
A:Accession: B49028
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-143 <TIM>
A:Cross-references: GB:S64473; NID:G236906; PIDN:AB20012.1; PID:G236907
A:Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell line
A>Note: Sequence extracted from NCBI backbone (NCBI:64473, NCBI:64472)
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match
Best Local Similarity 95.9%; Score 117; DB 2; Length 143;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYWSWIRQPRKGEWIG 19
DB 31 GYWSWIRQPRKGEWIG 49

RESULT 2
S26898
Ig heavy chain V region (clone DP-63, V(H)4.2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26898; S12420
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26898
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z1363; NID:G32944; PIDN:CA78233.1; PID:G32945
A:Experimental source: Clone DP-63
R:Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.
EMBO J. 8, 3741-3748, 1989
A:Title: The smaller human V(H) gene families display remarkably little polymorphism.
A:Reference number: S09421; MUID:90059975; PMID:2511001
A:Accession: S12420
A:Status: translation not shown
A:Molecule type: DNA

A;Residues: 1-97 <SANT>

A;Cross-references: EMBL:X56364

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C;Accession: S26806

R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.

Eur. J. Immunol. 22, 1075-1082, 1992

A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.

A;Reference number: S26800; MUID:92201299; PMID:1348029

A;Accession: S26806

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-97 <WEN>

C;Cross-references: EMBL:Z14242; NID:937716; PIDN:CA478611.1; PID:g1335377

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

RESULT 3

S26806

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C;Accession: S26806

R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.

Eur. J. Immunol. 22, 1075-1082, 1992

A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.

A;Reference number: S26800; MUID:92201299; PMID:1348029

A;Accession: S26806

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-97 <WEN>

C;Cross-references: EMBL:Z14242; NID:937716; PIDN:CA478611.1; PID:g1335377

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 93.4%; Score 114; DB 2; Length 97;

Best Local Similarity 94.7%; Pred. No. 2.1e-08;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 31 GYWSWIRPPGKGEWIG 49

RESULT 4

S26805

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C;Accession: S26805

R;Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.

Eur. J. Immunol. 22, 1075-1082, 1992

A;Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.

A;Reference number: S26800; MUID:92201299; PMID:1348029

A;Accession: S26805

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-97 <WEN>

C;Cross-references: EMBL:Z14241; NID:937714; PIDN:CA478610.1; PID:g1335376

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 93.4%; Score 114; DB 2; Length 97;

Best Local Similarity 94.7%; Pred. No. 2.1e-08;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 31 GYWSWIRPPGKGEWIG 49

RESULT 5

S14474

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000

C;Accession: S14474

R;van Es, J.H.; Gmelig Meyling, F.H.J.; van de Akker, W.R.M.; Aanstoot, H.; Derksen, R.I.

submitted to the EMBL Data Library, November 1990

A;Reference number: S14474

A;Accession: S14474

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-97 <ESJ>

C;Cross-references: EMBL:X56591; NID:937235; PIDN:CA439239.1; PID:g1335354

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97//Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 93.4%; Score 114; DB 2; Length 97;

Best Local Similarity 94.7%; Pred. No. 2.1e-08;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 31 GYWSWIRPPGKGEWIG 49

RESULT 6

S37454

Ig mu chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37454

R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.

submitted to the EMBL Data Library, September 1993

A;Title: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from

A;Reference number: S37453

A;Accession: S37454

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-106 <MC1>

C;Cross-references: EMBL:X75022; NID:g404311; PIDN:CA452330.1; PID:g758093

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

Query Match

Best Local Similarity 93.4%; Score 114; DB 2; Length 106;

Best Local Similarity 94.7%; Pred. No. 2.3e-08;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 9 GYWSWIRPPGKGEWIG 27

RESULT 7

JL0047

Ig heavy chain V region precursor (clone cR18) - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996

C;Accession: JL0047

R;Baer, R.; Forster, A.; Lavenir, I.; Rabblits, T.H.

J. Exp. Med. 167, 2011-2016, 1988

A;Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new

A;Reference number: JL0047; MUID:88288392; PMID:3133445

A;Accession: JL0047

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-122 <BAE>

A;Experimental source: T-cell line RPMI 8402

A;Note: this sequence belongs to the VH II subgroup

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;23-105//Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 114; DB 2; Length 122;
Best Local Similarity 94.7%; Pred. No. 2.7e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPGKGEWIG 19
Db 39 GYWSWIRQPPGKGEWIG 57

RESULT 8

S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S47010
R:Maumond, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
Submitted to the EMBL Data Library, July 1994
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bfr
A:Reference number: S47009
A:Accession: S47010
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <MAH>
A:Cross-references: EMBL:Z5492; NID:G517254; PIDN:CA04625.1; PID:G517255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:13-97/Domain: immunoglobulin homology <IMW>

Query Match 93.4%; Score 114; DB 2; Length 126;
Best Local Similarity 94.7%; Pred. No. 2.7e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPGKGEWIG 19
Db 31 GYWSWIRQPPGKGEWIG 49

RESULT 9

S78052
Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78052; S23717
R:Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78052
A:Molecule type: mRNA
A:Residues: 1-140 <HAR>
A:Cross-references: EMBL:X54441; NID:G37815; PIDN:CA03808.1; PID:G930118
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burratello, S.E.; Wilder, R.L.; Norking
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and H
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23717
A:Molecule type: mRNA
A:Residues: 15-111 <HAW>
A:Cross-references: EMBL:X54441
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:23-111/Domain: immunoglobulin homology <IMW>

Query Match 93.4%; Score 114; DB 2; Length 140;
Best Local Similarity 94.7%; Pred. No. 3.1e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPGKGEWIG 19
Db 45 GYWSWIRQPPGKGEWIG 63

RESULT 10
A49045
Ig heavy chain V region (anti-B cell autobody) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49045
R:Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaune, S.; Silvert
Eur. J. Immunol. 22, 1781-1788, 1992
A:Title: An anti-B cell autobody from Wiskott-Aldrich syndrome which recognizes I t
A:Reference number: A49045; MUID:92324290; PMID:1623923
A:Accession: A49045
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <GRI>
A:Cross-references: GB:S39381; NID:G250899; PIDN:AA022441.1; PID:G250900
A>Note: sequence extracted from NCBI backbone (NCBI:108088, NCBI:P:108089)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMW>

Query Match 93.4%; Score 114; DB 2; Length 140;
Best Local Similarity 94.7%; Pred. No. 3.1e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPGKGEWIG 19
Db 50 GYWSWIRQPPGKGEWIG 68

RESULT 11

GIHU2
Ig heavy chain precursor V-II region (ARH-77) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A02101
R:Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
Gene 33, 181-189, 1985
A:Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequ
A:Reference number: A02101; MUID:85205332; PMID:3922855
A:Accession: A02101
A:Molecule type: mRNA
A:Residues: 1-146 <KUD>
A:Cross-references: UNIPROT:P06331
A>Note: the sequence was determined from the differentiated gene
A>Note: the authors translated the codon GCG for residue 17 as Arg
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
A:Introns: 16/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <MAT>
F:20-117/Region: V segment
F:23-117/Domain: immunoglobulin homology <IMW>
F:35-117/Region: D segment
F:128-146/Region: J segment
F:42-115/Duplicate bonds: #status predicted

Query Match 91.0%; Score 111; DB 1; Length 146;
Best Local Similarity 89.5%; Pred. No. 8e-08;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRQPPGKGEWIG 19
Db 51 GYWSWIRQPPGKGEWIG 69

RESULT 12

S26902
Ig heavy chain V region (DP-67) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S26902

R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A>Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A/Reference number: S26885; MUID:93021117; PMID:1404388

A/Accession: S26902

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-98 <TOM>

A/Cross-references: EMBL:Z12367; NID:G32952; PIDN:CAV8237.1; PID:G32953

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 90.2%; Score 110; DB 2; Length 98;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 32 GYWGWIROPKGLKLEWIG 50

RESULT 13

Ig heavy chain V region (4.22) - human

C/Species: Homo sapiens (man)

C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C/Accession: S12421

R/Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.; Capra, J.D.

EMBO J. 8, 3741-3748, 1989

A>Title: The smaller human V(H) gene families display remarkably little polymorphism.

A/Reference number: S09421; MUID:9005975; PMID:2511001

A/Accession: S12421

A/Status: preliminary; translation not shown

A/Molecule type: DNA

A/Residues: 1-98 <SAN>

A/Cross-references: EMBL:X56365

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 90.2%; Score 110; DB 2; Length 98;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 32 GYWGWIROPKGLKLEWIG 50

RESULT 14

S30530

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C>Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C/Accession: S30530

R/Mariette, X.

submitted to the EMBL Data Library, October 1992

A/Reference number: S30520

A/Accession: S30530

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-123 <MAR>

A/Cross-references: EMBL:Z18316

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 90.2%; Score 110; DB 2; Length 123;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 32 GYWGWIROPKGLKLEWIG 50

RESULT 15

D2HUMA

Ig heavy chain V-II region (Mah) - human

C/Species: Homo sapiens (man)

C>Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 09-Jul-2004

C/Accession: A02099

R/Takahashi, N.; Telaar, D.; Debure, B.; Lin, L.C.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 79, 2850-2854, 1982

A>Title: Complete amino acid sequence of the delta heavy chain of human immunoglobulin

A/Reference number: A02099; MUID:8222235; PMID:6806818

A/Accession: A02099

A/Molecule type: protein

A/Residues: 1-129 <TAK>

A/Cross-references: UNIPROT:P01824

C/Comment: This chain was isolated from an Igd myeloma protein.

C/Genetics:

A/Gene: GDB:IGHV@

A/Cross-references: GDB:128528; OMIM:147070

A/Map position: 14q32.33-14q32.33

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-99/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 90.2%; Score 110; DB 1; Length 129;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19

DB 33 GYWGWIROPKGLKLEWIG 51

Search completed: April 25, 2005, 16:06:35

Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 15:48:23 ; Search time 176 Seconds

(without alignments)
55.281 Million cell updates/sec

Title: US-10-758-572-1

Sequence: 1 GYWSWIRQPGKGEWIG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|--------|--------------------|
| 1 | 114 | 93.4 | Q8WUX4 | Q8WUX4 homo sapien |
| 2 | 114 | 93.4 | Q6GMX5 | Q6GMX5 homo sapien |
| 3 | 114 | 93.4 | Q9BQ88 | Q9BQ88 homo sapien |
| 4 | 114 | 93.4 | Q9BU10 | Q9BU10 homo sapien |
| 5 | 114 | 93.4 | Q96AA6 | Q96AA6 homo sapien |
| 6 | 111 | 91.0 | Q7Z3Y6 | Q7Z3Y6 homo sapien |
| 7 | 111 | 91.0 | Q7Z3Y6 | Q7Z3Y6 homo sapien |
| 8 | 110 | 90.2 | Q9L173 | Q9L173 homo sapien |
| 9 | 108 | 88.5 | Q9L173 | Q9L173 homo sapien |
| 10 | 108 | 88.5 | Q9L173 | Q9L173 homo sapien |
| 11 | 108 | 88.5 | Q9L173 | Q9L173 homo sapien |
| 12 | 106 | 86.9 | Q6GMX6 | Q6GMX6 homo sapien |
| 13 | 104 | 85.2 | Q7Z3Y6 | Q7Z3Y6 homo sapien |
| 14 | 103 | 84.4 | Q8TC63 | Q8TC63 homo sapien |
| 15 | 100 | 82.0 | Q96EY0 | Q96EY0 homo sapien |
| 16 | 98 | 80.3 | Q96KX8 | Q96KX8 homo sapien |
| 17 | 96 | 78.7 | Q81ZD7 | Q81ZD7 homo sapien |
| 18 | 96 | 78.7 | Q95973 | Q95973 homo sapien |
| 19 | 95 | 77.9 | Q6P4I8 | Q6P4I8 homo sapien |
| 20 | 93 | 76.2 | Q6MZK7 | Q6MZK7 homo sapien |
| 21 | 92 | 75.4 | Q6GMX7 | Q6GMX7 homo sapien |
| 22 | 90 | 73.8 | Q7Z3Y9 | Q7Z3Y9 homo sapien |
| 23 | 88 | 72.1 | Q6B6Z0 | Q6B6Z0 oryctolagus |
| 24 | 88 | 72.1 | Q6B6Z2 | Q6B6Z2 oryctolagus |
| 25 | 88 | 72.1 | Q6B6Z2 | Q6B6Z2 oryctolagus |
| 26 | 87 | 71.3 | Q6B6Z2 | Q6B6Z2 oryctolagus |
| 27 | 87 | 71.3 | Q6B6Z2 | Q6B6Z2 oryctolagus |
| 28 | 86 | 70.5 | Q6B6Z2 | Q6B6Z2 oryctolagus |
| 29 | 85 | 69.7 | Q6B6Z2 | Q6B6Z2 oryctolagus |
| 30 | 84 | 68.9 | Q6B6Z2 | Q6B6Z2 oryctolagus |
| 31 | 84 | 68.9 | Q6B6Z2 | Q6B6Z2 oryctolagus |

| | | | | | | |
|----|----|------|-----|---|--------|--------------------|
| 32 | 84 | 68.9 | 119 | 2 | Q9GYZ2 | Q9GYZ2 schistosoma |
| 33 | 84 | 68.9 | 144 | 1 | Q9GYZ2 | Q9GYZ2 schistosoma |
| 34 | 84 | 68.9 | 225 | 2 | Q6P4I5 | Q6P4I5 xenopus lae |
| 35 | 84 | 68.9 | 479 | 2 | Q99M22 | Q99M22 mus musculu |
| 36 | 84 | 68.9 | 484 | 2 | Q8VEA0 | Q8VEA0 mus musculu |
| 37 | 83 | 68.0 | 117 | 1 | Q8VEA0 | Q8VEA0 mus musculu |
| 38 | 83 | 68.0 | 118 | 1 | Q8VEA0 | Q8VEA0 mus musculu |
| 39 | 82 | 67.2 | 99 | 2 | Q6B6T4 | Q6B6T4 oryctolagus |
| 40 | 82 | 67.2 | 101 | 2 | Q6B6T4 | Q6B6T4 oryctolagus |
| 41 | 82 | 67.2 | 105 | 2 | Q6B715 | Q6B715 oryctolagus |
| 42 | 82 | 67.2 | 116 | 1 | Q6B715 | Q6B715 oryctolagus |
| 43 | 82 | 67.2 | 117 | 1 | Q6B715 | Q6B715 oryctolagus |
| 44 | 82 | 67.2 | 119 | 1 | Q6B715 | Q6B715 oryctolagus |
| 45 | 82 | 67.2 | 119 | 1 | Q6B715 | Q6B715 oryctolagus |

ALIGNMENTS

| RESULT 1 | ID | Q8WUX4 | PRELIMINARY; | PRT; | 595 AA. |
|----------|------------------------------------------------------------------------|-----------------------------------------|--------------|--------|---------|
| AC | Q8WUX4 | Q8WUX4 | Q8WUX4 | Q8WUX4 | Q8WUX4 |
| DT | 01-MAR-2002 | (TREMBLrel. 20, Created) | | | |
| DT | 01-MAR-2004 | (TREMBLrel. 26, Last sequence update) | | | |
| DT | 01-MAR-2004 | (TREMBLrel. 26, Last annotation update) | | | |
| DE | Hypothetical protein. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | SEQUENCE FROM N.A. | | | | |
| RP | TISSUE=Lymph; | | | | |
| RC | MEBLIN=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; | | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., | | | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | | |
| RA | Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., | | | | |
| RA | Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | | | |
| RA | Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A., | | | | |
| RA | Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G., | | | | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | | | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., | | | | |
| RA | Krzywinski M.I., Skalska U., Small D.E., Schnerch A., Schein J.E., | | | | |
| RA | Jones S.J., Maitra M.A., | | | | |
| RT | "Generation and initial analysis of more than 15,000 full-length human | | | | |
| RT | and mouse cDNA sequences." | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Lymph; | | | | |
| RA | Strausberg R.L., | | | | |
| RA | Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases. | | | | |
| RL | EMBL, BC019235; AAH19235.2; - | | | | |
| DR | PIR, G34964; G34964. | | | | |
| DR | HSSP, P0161; IADQ. | | | | |
| DR | PIR, P0161; IADQ. | | | | |
| DR | SMART, PF07654; C1-set; 4. | | | | |
| DR | SMART, SMO0409; IG; 2. | | | | |
| DR | SMART, SMO0407; IGI; 4. | | | | |
| DR | SMART, SMO0406; IGV; 1. | | | | |
| DR | PROSITE, PS50835; IG LIKE; 5. | | | | |
| DR | PROSITE, PS00290; IG_MHC; UNKNOWN_3. | | | | |
| KW | Hypothetical protein. | | | | |
| SEQUENCE | 595 AA; 65290 MW; 0D4B5076545714E CRC64; | | | | |

Query Match 93.4%; Score 114; DB 2; Length 595;

Best Local Similarity 94.7%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
Db 57 GYWSWIRPPGKGEWIG 75

RESULT 2

Q6GMX5 PRELIMINARY; PRT; 597 AA.
ID Q6GMX5
AC Q6GMX5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AAH73767.1; -
DR InterPro; IPR003599; IG -
DR InterPro; IPR007110; IG -like.
DR InterPro; IPR003597; IG -cl.
DR InterPro; IPR003006; IG -MHC.
DR InterPro; IPR003596; IG -v.
DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG LIKE; 5.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.

QY SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED5230 CRC64;

Query Match 93.4%; Score 114; DB 2; Length 597;
Best Local Similarity 94.7%; Pred. No. 2.4e-07;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
Db 50 GYWSWIRPPGKGEWIG 68

RESULT 3

Q9B0B8 PRELIMINARY; PRT; 597 AA.
ID Q9B0B8
AC Q9B0B8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -
DR HSSP; P01861; IADO.
DR InterPro; IPR007110; IG -like.
DR InterPro; IPR003597; IG -cl.
DR InterPro; IPR003006; IG -MHC.
DR InterPro; IPR003596; IG -v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PSS0835; IG LIKE; 5.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_3.
KW SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 93.4%; Score 114; DB 2; Length 597;
Best Local Similarity 94.7%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPGKGEWIG 19
Db 50 GYWSWIRPPGKGEWIG 68

RESULT 4

Q9B0B8 PRELIMINARY; PRT; 597 AA.
ID Q9B0B8
AC Q9B0B8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Collins F.S., Grouse L.H., Derge J.G.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullany S.J.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Straubeberg R.;
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sect; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65274 MW; 2DFAFB7E055851 CRC64;

Query Match 93.4%; Score 114; DB 2; Length 597;
Best Local Similarity 94.7%; Pred. No. 2.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPKGEWIG 19
DB 50 GYWSWIRPPKGEWIG 68

RESULT 5
096AA6 PRELIMINARY; PRT; 625 AA.
ID 096AA6
AC 096AA6
DT 01-DEC-2001 (TREMBlrel. 19; Created)
DT 01-DEC-2001 (TREMBlrel. 19; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Collins F.S., Grouse L.H., Derge J.G.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer C.F.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Straubeberg R.;
RA Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.2; -.
DR PIR; S15590; S15590.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sect; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 4.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBE CRC64;

Query Match 93.4%; Score 114; DB 2; Length 625;
Best Local Similarity 94.7%; Pred. No. 2.5e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWSWIRPPKGEWIG 19
DB 57 GYWSWIRPPKGEWIG 75

RESULT 6
0723Y6 PRELIMINARY; PRT; 116 AA.
ID 0723Y6
AC 0723Y6
DT 01-OCT-2003 (TREMBlrel. 25; Created)
DT 01-OCT-2003 (TREMBlrel. 25; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE Rearranged VH4-34 V gene segment (Fragment).
GN Name=VH4-34;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hodgkin Lymphoma;
RA Tinguely M., Rosenquist R., Sundtrem C., Amini R.M., Kuipers R.,
RA Hansmann M.L., Branninger A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564425; CAD92032.1; -.
DR HSP; P18532; IKCV.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 116 AA; 12902 MW; CE3DBA846616C908 CRC64;
```

Query Match 91.0%; Score 111; DB 2; Length 116;
Best Local Similarity 89.5%; Pred. No. 1.3e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRPPGKGEWIG 19
|||||
Db 31 GYWSWIRPPGKGEWIG 49

RESULT 7
ID HV21 HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JUN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region."
RL Gene 33:181-189(1985).
RL PIR: A02101; GIHMH2.
DR HSSP; P01825; 7PAB.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.
FT DOMAIN 20 117 V segment.
FT DOMAIN 118 127 D segment.
FT DOMAIN 128 146 U segment.
FT DISULFID 42 115 By similarity.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 807FD52BB218171F CRC64;

Query Match 91.0%; Score 111; DB 1; Length 146;
Best Local Similarity 89.5%; Pred. No. 1.6e-07;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWSWIRPPGKGEWIG 19
|||||
Db 51 GYWSWIRPPGKGEWIG 69

RESULT 8
ID HV2F HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP MEDLINE=82222235; PubMed=6806818;

RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT immunoglobulin D."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -1- MISCELLANEOUS: This chain was isolated from an Igd myeloma
CC protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR: A02099; D2HUMA.
DR HSSP; P01820; 1G7J.
DR Glycosylated; P01824; -.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_LIKE.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 113
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE5119 CRC64;

Query Match 90.2%; Score 110; DB 1; Length 129;
Best Local Similarity 89.5%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYWSWIRPPGKGEWIG 19
|||||
Db 33 GYWSWIRPPGKGEWIG 51

RESULT 9
ID Q9UL73 PRELIMINARY; PRT; 119 AA.
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig_LIKE.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EAOBE CRC64;

Query Match 88.5%; Score 108; DB 2; Length 119;
Best Local Similarity 94.4%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YWSWIRPPGKGEWIG 19
|||||
Db 32 YWSWIRPPGKGEWIG 49

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RESULT 10
O66SX2 PRELIMINARY; PRT; 139 AA.
ID O66SX2;
AC O66SX2;
DT 01-JUN-2003 (TRENBLREL. 24, Created)
DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Full-length cDNA clone CS00L004YM19 of B cells (Ramos cell line) of
DE Homo sapiens (human).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Smith, S.M.0406; IG, 1.
DR SMART; PS50835; IG LIKE; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER
SQ SEQUENCE 139 AA; 15573 MW; 7D1E2302410E4F8C CRC64;

Query Match 88.5%; Score 108; DB 2; Length 139;
Best Local Similarity 94.4%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

O66SX2 PRELIMINARY; PRT; 476 AA.
ID O66SX2;
AC O66SX2;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038959;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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RA Krzywnski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.L.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG LIKE.
DR InterPro; IPR003597; IG CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sec; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 88.5%; Score 108; DB 2; Length 476;
Best Local Similarity 94.4%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

O66MX6 PRELIMINARY; PRT; 465 AA.
ID O66MX6;
AC O66MX6;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038959;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
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RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 86.9%; Score 106; DB 2; Length 465;
Best Local Similarity 89.5%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYWSWIRPPGKGEWIG 19
Db 50 GYWSWIRPPGKGEWIG 68

RESULT 13
Q72374 PRELIMINARY; PRT; 492 AA.
ID 072374
AC 072374
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Podo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX38077; CAD98001.1; -.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
KM NON TER
FT 1
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 85.2%; Score 104; DB 2; Length 492;
Best Local Similarity 88.9%; Pred. No. 4.8e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YYWSWIRPPGKGEWIG 19
Db 65 YYWSWIRPPGKGEWIG 82

RESULT 14
Q8TC63 PRELIMINARY; PRT; 473 AA.
ID 08TC63

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AC 08TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
RA Krausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsien F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Millaby S.J.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0196; COPPER BLUE; UNKNOWN_1.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 473 AA; 51986 MW; E29920B9BA369F5 CRC64;

Query Match 84.4%; Score 103; DB 2; Length 473;
Best Local Similarity 83.3%; Pred. No. 6.3e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YYWSWIRPPGKGEWIG 19
Db 60 YYWSWIRPPGKGEWIG 77

RESULT 15
Q96EY0 PRELIMINARY; PRT; 620 AA.
ID 096EY0
AC 096EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uscin T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raza S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSP; P01820; 1G7J.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

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